FIGURE 1

GAAF: 5'-GCGATAGGTACCGCCATGGGAGTGAGGCACCCGCCCTGCTCCC-3'

GAAR: 5'-GCGATACTCGAGTCAACACCAGCTGACGAGAAACTGCTCTCCC-3'

FIGURE 2

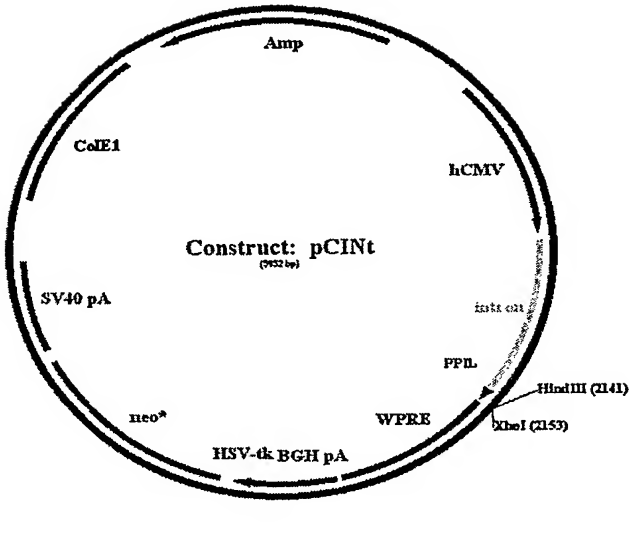
Amp
ColE1
hCMV
Construct: pCINt
SV40 pA
PPIL
HindIII (2141)
XhoI (2153)
neo*
WPRE
HSV-tk BGH pA
100

FIGURE 3

atgaaagggtccctcctgctgctgctggtgtcaaacctgctcctgtgccagagcgggtcc
M K G S L L L L L V S N L L L C Q S G S
ggagccggggcccacatcctactccatgatttcctgctggttccccgagagctgagtggc
G A G A H I L L H D F L L V P R E L S G
tcctccccagtcctggaggagactcacccagctcaccagcagggagccagcagaccaggg
S S P V L E E T H P A H Q Q G A S R P G
ccccgggatgcccaggcacaccccggccgtcccagagcagtgcccacacagtgcgacgtc
P R D A Q A H P G R P R A V P T Q C D V
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P P N S R F D C A P D K A I T Q E Q C E
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A R G C C Y I P A K Q G L Q G A Q M G Q
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P W C F F P P S Y P S Y K L E N L S S S
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E M G Y T A T L T R T T P T F F P K D I
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L T L R L D V M M E T E N R L H F T I K
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D P A N R R Y E V P L E T P R V H S R A
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P S P L Y S V E F S E E P F G V I V H R
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Q L D G R V L L N T T V A P L F F A D Q
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F L Q L S T S L P S Q Y I T G L A E H L
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S P L M L S T S W T R I T L W N R D L A
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G S A H G V F L L N S N A M D V V L Q P
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R Q V V E N M T R A H F P L D V Q W N D
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L D Y M D S R R D F T F N K D G F R D F
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G V F I T N E T G Q P L I G K V W P G S
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T A F P D F T N P T A L A W W E D M V A
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E F H D Q V P F D G L W I D M N E P S N
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F I R G S E D G C P N N E L E N P P Y V
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P G V V G G T L Q A A T I C A S S H Q F
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L S T H Y N L H N L Y G L T E P I A S H
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R A L V K A R G T R P F V I S R S T F A
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G H G R Y A G H W T G D V W S S W E Q L
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A S S V P E I L Q F N L L G V P L V G A
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D V C G F L G N T S E E L C V R W T Q L
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G A F Y P F M R N H N S L L S L P Q E P
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Y S F S E P A Q Q A M R K A L T L R Y A
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L L P H L Y T L F H Q A H V A G E T V A
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R P L F L E F P K D S S T W T V D H Q L
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L W G E A L L I T P V L Q A G K A E V T
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G Y F P L G T W Y D L Q T V P I E A L G
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S L P P P P A A P R E P A I H S E G Q W
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P L Q G P G L T T T E S R Q Q P M A L A
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V A L T K G G E A R G E L F W D D G E S
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L E V L E R G A Y T Q V I F L A R N N T
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I V N E L V R V T S E G A G L Q L Q K V
actgtcctgggcgtggccacggcgccccagcaggtcctctccaacggtgtccctgtctcc
T V L G V A T A P Q Q V L S N G V P V S
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N F T Y S P D T K V L D I C V S L L M G
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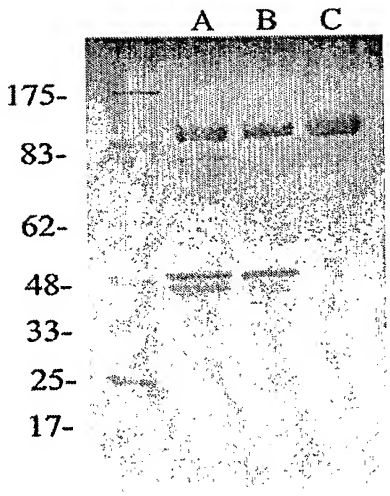
E Q F L V S W C -

FIGURE 4

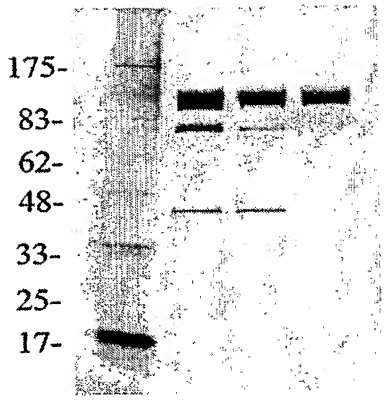
A) Blue Eluate

B) Q Eluate

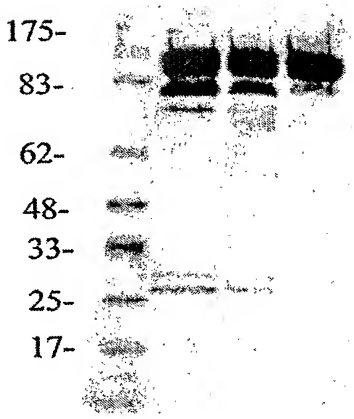
C) Phe Eluate



Commassie 5ug BM103/lane



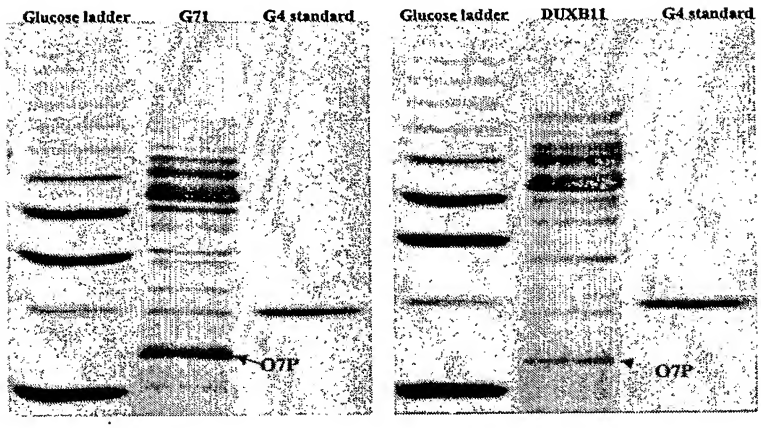
Ag+ 5ug BM103/lane



Western (1:5000) Primary
0.5ug BM103 / lane

FIGURE 5

FACE profiles for GAA from G715 and DUXB11



O7P 19% of total oligosaccharide profile

O7P 6.7% of total oligosaccharide profile

FIGURE 6

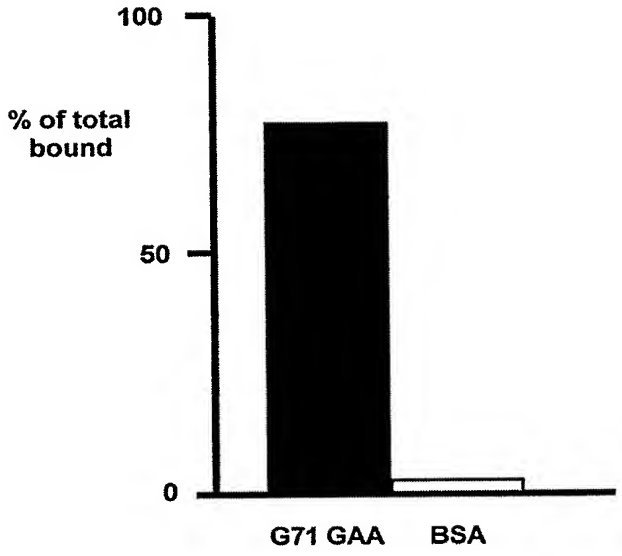
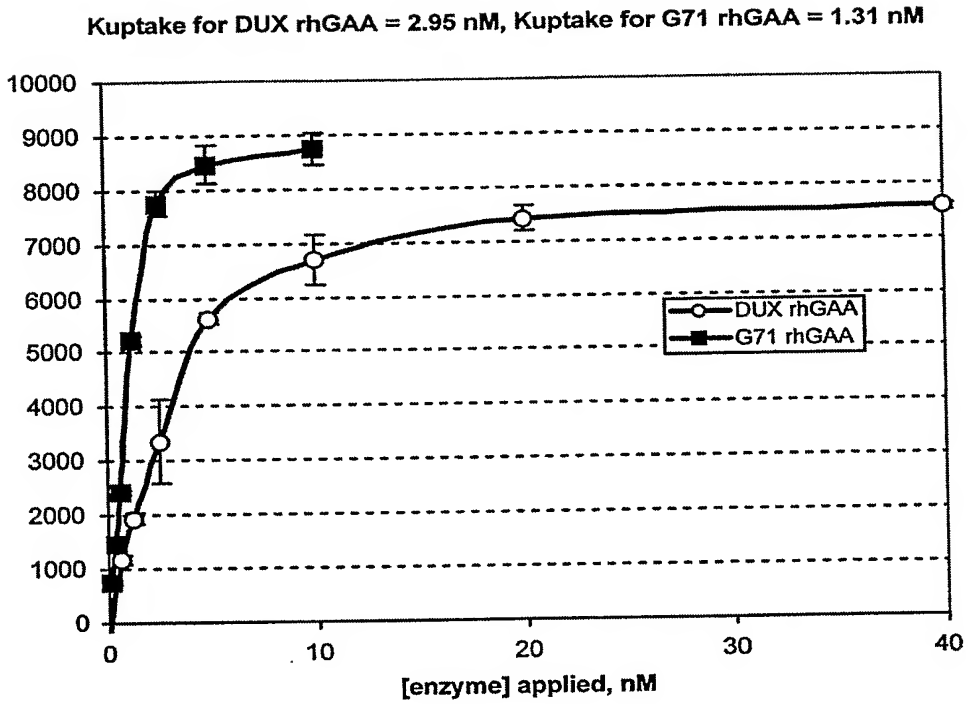


FIGURE 7


Kuptake for DUX rhGAA = 2.95 nM, Kuptake for G71 rhGAA = 1.31 nM
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
0
10
20
30
40
[enzyme] applied, nM
DUX rhGAA
G71 rhGAA